


```

QY 121 MKAVLNKDGVNACILPLQIDRDGSGNPOPLVNAOCTDDYRGHSALHIAIEKRSIQCVK 180
    |||
DB 121 MKAVLNKDGVNACILPLQIDRDGSGNPOPLVNAOCTDDYRGHSALHIAIEKRSIQCVK 180
QY 181 LVVENGANYHARACGRPFQKQCTCFYFGEPLSLAACKRMQDVSYLLENPHQPASLOA 240
    |||
DB 181 LVVENGANYHARACGRPFQKQCTCFYFGEPLSLAACKRMQDVSYLLENPHQPASLOA 240
QY 241 TDSQGNVTHALVMIISDNSAENIALVTSMDGLQAGARLCPVQLEDIRNLQDLTPKL 300
    |||
DB 241 TDSQGNVTHALVMIISDNSAENIALVTSMDGLQAGARLCPVQLEDIRNLQDLTPKL 300
QY 301 AAKEGKIEIFRHILOREFSGLSLSRKFTWCYGPVRSIYDLASVSCSENSVLEIIAF 360
    |||
DB 301 AAKEGKIEIFRHILOREFSGLSLSRKFTWCYGPVRSIYDLASVSCSENSVLEIIAF 360
QY 361 HCKSPRHRRVYLEPLNKLQAKMDLLIPKFLNLCNLTYMFIFPAVAYHOPTLKKQAA 420
    |||
DB 361 HCKSPRHRRVYLEPLNKLQAKMDLLIPKFLNLCNLTYMFIFPAVAYHOPTLKKQAA 420
QY 421 PHLKAEGVNSMLTGHILLGSIYLLVGOAMYFMRHRVFIWISFIDSYFEILLFQALL 480
    |||
DB 421 PHLKAEGVNSMLTGHILLGSIYLLVGOAMYFMRHRVFIWISFIDSYFEILLFQALL 480
QY 481 TVVSOVLCFLAIEWYLPPLVLSALVGLMNLVYTRGFQHTGIYSVMIOKVILRDLRFL 540
    |||
DB 481 TVVSOVLCFLAIEWYLPPLVLSALVGLMNLVYTRGFQHTGIYSVMIOKVILRDLRFL 540
QY 541 IYLVFLGFPAVALVLSQEAAMREAPTGPNATESVQPMQEDGNGAOYRGILLEASLEL 600
    |||
DB 541 IYLVFLGFPAVALVLSQEAAMREAPTGPNATESVQPMQEDGNGAOYRGILLEASLEL 600
QY 601 FKTTIGMGLAFQEOJHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
    |||
DB 601 FKTTIGMGLAFQEOJHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAISVLEMENGYWMCRRKORAGVMLTVGTRPDGSPDERMCFRVEEYNNMASWEGTLPT 720
    |||
DB 661 KLOKAISVLEMENGYWMCRRKORAGVMLTVGTRPDGSPDERMCFRVEEYNNMASWEGTLPT 720
QY 721 LCEDPGAGVPTLENPVLASPKEDDGAASEENYVPVOLLQSN 764
    |||
DB 721 LCEDPGAGVPTLENPVLASPKEDDGAASEENYVPVOLLQSN 764

RESULT 2
QY670 PRELIMINARY: PRT: 764 AA.
AC QY670;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE VANILLOID RECEPTOR-LIKE PROTEIN.
GN VRL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Garcia R.L., Delmas P., Cesare P., England S., Liapi A., Wood J.N.;
RT "Cloning and functional expression of VRL, a vanilloid receptor-like
RT gene."
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF103906; AAD41724.1; -.
DR InterPro: IPR002110; -.
DR pfam: PF00023; ank. 3.
DR PROSITE: PS50088; ANK_REPEAT. 1.
DR PROSITE: PS50297; ANK_REGION; 1.
DR SMART: SM00248; ANK; 1.
KW Receptor.

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SQ SEQUENCE 764 AA: 86053 MW: AF9DEBF495EB43A0 CRC64:
Query Match 98.5%; Score 3945; DB 4; Length 764;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 750; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 MSPSSSPVFRLETTLDGQEDGSEADRGKIDFGSGLPMPESQFQGEDRRKFAPIRVNLY 60
    |||
DB 1 MSPSSSPVFRLETTLDGQEDGSEADRGKIDFGSGLPMPESQFQGEDRRKFAPIRVNLY 60
QY 61 RKGTGASQDPNFRDRLFNNAVSRGVPEPDLAGPEYLSKTYLLTDEYTBGSTKTL 120
    |||
DB 61 RKGTGASQDPNFRDRLFNNAVSRGVPEPDLAGPEYLSKTYLLTDEYTBGSTKTL 120
QY 121 MKAVLNKDGVNACILPLQIDRDGSGNPOPLVNAOCTDDYRGHSALHIAIEKRSIQCVK 180
    |||
DB 121 MKAVLNKDGVNACILPLQIDRDGSGNPOPLVNAOCTDDYRGHSALHIAIEKRSIQCVK 180
QY 181 LVVENGANYHARACGRPFQKQCTCFYFGEPLSLAACKRMQDVSYLLENPHQPASLOA 240
    |||
DB 181 LVVENGANYHARACGRPFQKQCTCFYFGEPLSLAACKRMQDVSYLLENPHQPASLOA 240
QY 241 TDSQGNVTHALVMIISDNSAENIALVTSMDGLQAGARLCPVQLEDIRNLQDLTPKL 300
    |||
DB 241 TDSQGNVTHALVMIISDNSAENIALVTSMDGLQAGARLCPVQLEDIRNLQDLTPKL 300
QY 301 AAKEGKIEIFRHILOREFSGLSLSRKFTWCYGPVRSIYDLASVSCSENSVLEIIAF 360
    |||
DB 301 AAKEGKIEIFRHILOREFSGLSLSRKFTWCYGPVRSIYDLASVSCSENSVLEIIAF 360
QY 361 HCKSPRHRRVYLEPLNKLQAKMDLLIPKFLNLCNLTYMFIFPAVAYHOPTLKKQAA 420
    |||
DB 361 HCKSPRHRRVYLEPLNKLQAKMDLLIPKFLNLCNLTYMFIFPAVAYHOPTLKKQAA 420
QY 421 PHLKAEGVNSMLTGHILLGSIYLLVGOAMYFMRHRVFIWISFIDSYFEILLFQALL 480
    |||
DB 421 PHLKAEGVNSMLTGHILLGSIYLLVGOAMYFMRHRVFIWISFIDSYFEILLFQALL 480
QY 481 TVVSOVLCFLAIEWYLPPLVLSALVGLMNLVYTRGFQHTGIYSVMIOKVILRDLRFL 540
    |||
DB 481 TVVSOVLCFLAIEWYLPPLVLSALVGLMNLVYTRGFQHTGIYSVMIOKVILRDLRFL 540
QY 541 IYLVFLGFPAVALVLSQEAAMREAPTGPNATESVQPMQEDGNGAOYRGILLEASLEL 600
    |||
DB 541 IYLVFLGFPAVALVLSQEAAMREAPTGPNATESVQPMQEDGNGAOYRGILLEASLEL 600
QY 601 FKTTIGMGLAFQEOJHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
    |||
DB 601 FKTTIGMGLAFQEOJHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAISVLEMENGYWMCRRKORAGVMLTVGTRPDGSPDERMCFRVEEYNNMASWEGTLPT 720
    |||
DB 661 KLOKAISVLEMENGYWMCRRKORAGVMLTVGTRPDGSPDERMCFRVEEYNNMASWEGTLPT 720
QY 721 LCEDPGAGVPTLENPVLASPKEDDGAASEENYVPVOLLQSN 764
    |||
DB 721 LCEDPGAGVPTLENPVLASPKEDDGAASEENYVPVOLLQSN 764

RESULT 3
QY671 PRELIMINARY: PRT: 756 AA.
AC QY671;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE GROWTH FACTOR REGULATED CALCIUM CHANNEL.
GN VRL1 OR GRC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

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[1]
RN SEQUENCE FROM N.A.
RP STRAIN-C57 BLACK-6; TISSUE=SPLEEN;
RA Kanazaki M., Zhang Y., Kojima I.;
RT "Growth factor regulated calcium channel."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021665; BAA78478.1; -
DR MGD; MGI:1341836; Vrl1.
DR InterPro: IPR002110; -
DR InterPro: IPR002111; -
DR Pfam: PF00023; ank; 3.
DR PROSITE: PSS0088; ANK_REPEAT; 1.
DR PROSITE: PSS0297; ANK_REPEAT_REGION; 1.
DR SMART; SM00248; ANK; 1.
SQ SEQUENCE 756 AA; 85964 MW; 4C037D0F6066EFAC CRC64;

Query Match 78.9%; Score 3159; DB 11; Length 756;
Best Local Similarity 80.3%; Pred. No. 7.2e-241;
Matches 615; Conservative 55; Mismatches 84; Indels 12; Gaps 5;

QY 1 MTSSSSPVFLRLETLDDGQEDGSEADGKLDGSGLPMEQFQGEDRKFPQIRVNLNY 60
DB 1 MTSASNPAPFLRLETSDDGEGSAEVNKGK---NEPPMESPFQGEDRNFSPQIKVNLNY 56
QY 61 RKGTGASQDPNFRDRDLFNAVSRGVPEDLAQLPEYLSKTSKYLTDSEYEGSTGKTC 120
DB 57 RKGLGPPSQDPPNRDRDLRFVSVRGVPEELTGLLEYLRKSKYLTDSATYEGSTGKTC 116
QY 121 MKAVLNLKQGVNACILPLQIDRDSGNPQPLVNAQCTDDYRGSHALHIAIEKRSLOCVK 180
DB 117 MKAVLNLQDQGVNACILPLQIDRDSGNPQPLVNAQCTDEYRGSHALHIAIEKRSIMC 176
QY 181 LTVNGANVHARACGRPFQKQGCYFGEPLSLAACKTQMDVVSYLENPHQPASQQA 240
DB 177 LTVNGANVHARACGRPFQKQGCYFGEPLSLAACKTQMDVVSYLENPHQPASLEA 236
QY 241 TDSQGNVTLHALVMIISDNSAENIALVTSMYDGLQAGARLCPVQLEDIRNLQDLPKL 300
DB 237 TDSIGNVTLHALVMIADNSPENSALVIMYDSLQMGARLCPVQLEDICHHQGITPKL 296
QY 301 AAKGKTEIFRHLIQREFSGT-SHLSRKFTWCYGVAVRSVLYDLASVDSCEENVLEIIA 359
DB 297 AAKGKTEIFRHLIQREFSGT-SHLSRKFTWCYGVAVRSVLYDLASVDSCEENVLEIIA 356
QY 360 FHCSPPHRRMVLEPLNKLQAKWDLLIPKFLNPLCNLYMFLFPAVAHQPILKQQA 419
DB 357 FHCSPPHRRMVLEPLNKLQAKWDLLIPKFLNPLCNLYMFLFPAVAHQPILKQQA 416
QY 420 APHLKAEGNSMLTGHLLILGGLYLLVQGLWFWRHVFIMISFIDSEIFELFOAL 479
DB 417 IPSSKATFGSDMLLGHLLILGGLYLLVQGLWFWRHVFIMISFIDSEIFELFOAL 476
QY 480 LTVVSOVLCFLAIWYLPPLVSALVGLWNLVYTRGFQHTGTVSMIOKVILRDLEFL 539
DB 477 LTVLSOVLRFETEMWYLPPLVSSLVGLWNLVYTRGFQHTGTVSMIOKVILRDLEFL 536
QY 540 LTVVLFEGFVALVLSQEAWRPEAPTPGKATESVQPMQEGDEGNAQAGRTLEASLE 599
DB 537 LTVVLFEGFVALVLSQEAWRPEAPTPGKATESVQPMQEGDEGNAQAGRTLEASLE 594
QY 600 LKFTTIGMGLAFQEOQLFRGMVLLLLAVLVLTYYILLNMLIAMSETVSVATDSMSI 659
DB 595 LKFTTIGMGLAFQEOQLFRGMVLLLLAVLVLTYYILLNMLIAMSETVSVATDSMSI 654
QY 660 WKLOKALISVLEMENGYMCCRKQ-RAGVMLTVGTRKPDGSPDERKCFRVEEVNMAWQOTL 718
DB 655 WKLOKALISVLEMENGYMCCRKRRHAGRLKLVKGDGQIPDERKCFRVEEVNMAWQOTL 714
QY 719 PTLCEPDSGAGVPRTELENPVLASPKKEDEGASBENVVYVQVLLQSN 764
DB 715 PTLSEDPGAGITGYKKNP-----SKPEKNSASEBHLPLQVLOSH 756

RESULT 4
ID 09WMD2 PRELIMINARY; PRT: 761 AA.
AC 09WMD2;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VANILLOID RECEPTOR-LIKE PROTEIN 1.
GN VRL-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=99215558; PubMed=10201375;
RA Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;
RT "A capsaicin-receptor homologue with a high threshold for noxious
heat";
RL Nature 398:436-441(1999).
DR EMBL; AF129113; AAD26364.1; -
DR InterPro: IPR002110; -
DR InterPro: IPR002111; -
DR Pfam: PF00023; ank; 3.
DR PROSITE: PSS0088; ANK_REPEAT; 1.
DR PROSITE: PSS0297; ANK_REPEAT_REGION; 1.
DR SMART; SM00248; ANK; 1.
KW Receptor.
SQ SEQUENCE 761 AA; 86689 MW; 46A281183EB672F CRC64;

Query Match 76.2%; Score 3051.5; DB 11; Length 761;
Best Local Similarity 77.7%; Pred. No. 2.2e-222;
Matches 598; Conservative 62; Mismatches 93; Indels 17; Gaps 7;

QY 1 MTSSSSPVFLRLETLDDGQEDGSEADGKLDGSGLPMEQFQGEDRKFPQIRVNLNY 60
DB 1 MTSASNPAPFLRLETSDDGEGNAEVNKGKQF---PPMESPFQGEDRNFSPQIKVNLNY 56
QY 61 ---RKGTGA-SQDPNFRDRDLFNAVSRGVPEDLAQLPEYLSKTSKYLTDSEYEGST 115
DB 57 IKRPPKNTSAPSOEPPDRDLRFVSVRGVPEELTGLLEYLRNMSKYLTDSEYEGST 116
QY 116 KGTCLMKRVNLKQGVNACILPLQIDRDSGNPQPLVNAQCTDDYRGSHALHIAIEKRS 175
DB 117 KGTCLMKRVNLKQGVNACILPLQIDRDSGNPQPLVNAQCTDEYRGSHALHIAIEKRS 176
QY 176 LQCVKLTVENGANVHARACGRPFQKQGCYFGEPLSLAACKTQMDVVSYLENPHQ 235
DB 177 LQCVKLTVENGANVHARACGRPFQKQGCYFGEPLSLAACKTQMDVVSYLENPHQ 236
QY 236 ASLQATDSQGNVTLHALVMIISDNSAENIALVTSMYDGLQAGARLCPVQLEDIRNLQD 295
DB 237 ASLQATDSQGNVTLHALVMIADNSPENSALVIMYDSLQMGARLCPVQLEDISNHQ 296
QY 296 TPPLKAAEGKTEIFRHLIQREFSGT-SHLSRKFTWCYGVAVRSVLYDLASVDSCEENV 354
DB 297 TPPLKAAEGKTEIFRHLIQREFSGT-SHLSRKFTWCYGVAVRSVLYDLASVDSCEENV 356
QY 355 LEIIAFHCKSPHRRMVLEPLNKLQAKWDLLIPKFLNPLCNLYMFLFPAVAHQP 414
DB 357 LEIIAFHCKSPHRRMVLEPLNKLQAKWDLLIPKFLNPLCNLYMFLFPAVAHQP 416
QY 415 LKQOAPHLKAEGNSMLTGHLLILGGLYLLVQGLWFWRHVFIMISFIDSEIFEL 474
DB 417 LKQOAPHLKAEGNSMLTGHLLILGGLYLLVQGLWFWRHVFIMISFIDSEIFEL 476
QY 475 LFOALLTVVSOVLCFLAIWYLPPLVSALVGLWNLVYTRGFQHTGTVSMIOKVILRD 534
DB 477 LFOALLTVVSOVLCFLAIWYLPPLVSALVGLWNLVYTRGFQHTGTVSMIOKVILRD 536

[illegible]

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RESULT      5
090YH8      ID      090YH8      PRELIMINARY;      PRT;      761 AA.
AC      090YH8;
DT      01-MAY-2000 (TREMblrel, 13, Created)
DT      01-MAY-2000 (TREMblrel, 13, Last sequence update)
DT      01-MAR-2001 (TREMblrel, 16, Last annotation update)
DE      STRETCH ACTIVATED_CHANNEL 2B.
GN      RSAC2B.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
      ||
      SEQUENCE FROM N.A.
RA      RNP
RA      Ishibashi K.;
RT      "Molecular cloning of a stretch activated channel from rat kidney.";
RL      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AB029330; BAA8637.1; -.
DR      InterPro: IPR002110; -.
DR      InterPro: IPR002111; -.
DR      Pfam: PF00023; ank; 3.
DR      PROSITE: PS50088; ANK_REPEAT; 1.
DR      PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR      SMART: SM00248; ANK_1
SO      SEQUENCE      761 AA;      86705 MW;      8977CDEID535IEC8 CRC64;

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Query Match	76.0%	Score 3041.5	DB 11	Length 761
Best Local Similarity	77.58%	Pred. No. 1.4e-231		
Matches 597	Conservative 62	Mismatches 94	Indels 17	Gaps 7
QY	1	MTSPSSPVFRLETTLDGGOEDGSEADRGKLDGSGSLPMEISOFOGEDRFAFOIRVNLNY	60	
		: : :		
Db	1	MTSASSPPAFRLRLETSIDGDEGNAEYNNKKQE-----PPMESPFOREDRNRSSPQIKVNLNF	56	
QY	61	----RKGTGA--SQDPNPNRDRDLFNVAWSRGVPEDLAILEYLSKTSKYLTDESYTEGST	115	
Db	57	IKRPKNTSAPSSQOEPDRDFRDRLFSVWSRGVPEELTGLLEFLRNNSKYLFTSAYTEGST	116	
QY	116	GKTCMKRVNLNKDGVNACIIPLTLOIDDSGQNPOLVNAQCCTDDYVYRGSAHIAIEKRS	175	
Db	117	GKTCMKRVNLNKDGVNACIIMPLOIDDSGNPKLVNNAQCCTDEYVYQGSALHIAIEKRS	176	
QY	176	LQCVLLVENGANVYARACGRFFQGGCTCFYFGEPLSLIACCTKQMDVSVYLENPHOP	235	
Db	177	LQCVLLVENGADVHLRACGRFFQKHQGTCTFFGELPLSLIACCTKQMDVYVYLLLENPHOP	236	
QY	236	ASLQATDSQGNVTIHALVWISDSNAENTALVTSMTDGLLQAGARLCPTVQLEDIRNLQDL	295	
Db	237	ASLEATDSLGVTIHALVWIDNSPENSALVTHMTDGLLQMGARLCPTVQLEIRSNHQL	296	
QY	296	TPKLAAAEGRKLEIFRHLIQREFSG--LSHLSKFTFWCGYPRVSVLYDLASVDSCEENV	354	
Db	297	TPKLAAAEGRKLEIFRHLIQREFSGPYOPLSKFTFWCGYPRVSVLYDLASVDSCEENV	356	

0y	365	LEIAFHCKSPHRRHMYVLEPLNKLLOAKMDLLPKFELNFCULYMFJFTAAVYOPT	414
Db	357	LEIIAIFHCKSPHRRHMYVLEPLNKLLOAKMDLLPKFELNFCULYMFJFTAAVYOPT	416
0y	415	..KKQAAPLKAEEVNSMMLTGHIILLLGGIYLLVGOUMYFMRHHVFIMWISFIDSYEILF	474
Db	417	LDQPAIPSKATFGBSMMLGGHILLLGGIYLLVGOUMYFMRRLFIWISFIDSYEILF	476
0y	475	LFQALLVYVSOYLCFLAEMYLPLVLSALVGMNLLYTRRGFOHTGYSVMLOKYLKD	534
Db	477	LLQALLTVLSOYLFEMETEWLPLTVLSLVGMNLLYTRRGFOHTGYSVMLOKYLKD	536
0y	535	LLRFLLLVYLVLFGRFAVALVLSQEAURPEAPRTPNATPESVQPMEGEDGNGAOYRGIL	594
Db	537	LLRFLVYLVYLVLFGRFAVALVLSQEAURPKAPREDNNSTVYBQPPVGOEE--PAPYRSIL	594
0y	595	EASLELFFKTIGMELAFQEDLHNRGVULLLLAYLVLLYLLLNMLIALMSETVNSVAT	654
Db	595	DASLELFFKTIGMELAFQEDLHNRGVULLLLAYLVLLYLLLNMLIALMSEFVNHAD	654
0y	655	DSWSIMWIKOKAISYLEMBNGTYMC--RKKORAGWMLYGTYPDQSPDERKCFRYAEVNMAS	713
Db	655	NSWSIMWIKOKAISYLEMBNGTYMCRRKKHREGRLKAGTGGDGTDPDERMCFRYAEVNMMA	714
0y	714	MEQTLPTLCEDBPSGAGVPRILENVULASPRKEDDGSSENVYUVOULL	763
Db	715	WEKTLPTLSEDPSPGTLGNKNKPT--SKPGNSASSEEDHNPLOYOVS	760

RESULT	6		
Q9JMT8			
ID	Q9JMT8	PRELIMINARY;	PRT; 762 AA.
AC	Q9JMT8;		
DT	01-OCT-2000 (TReMBLrel. 15, Created)		
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TReMBLrel. 16, Last annotation update)		
DE	ION CHANNEL.		
OS	Rattus norvegicus (Rat).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
	(1)		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=KIDNEY;		
RA	Suzuki M.;		
RT	"Ion channel.";		
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB022332; BAA93435.1; -		
DR	InterPro; IPR002110; -		
DR	InterPro; IPR002111; -		
DR	Pfam; PF000023; ank. 3.		
DR	PROSITE; PSS00088; ANK_REPEAT. 1.		
DR	PROSITE; PSS0297; ANK_REPEAT_REGION. 1.		
DR	SMART; SM00248; ANK. 1.		
Q9	SEQUENCE 762 AA; 86767 MW; CE0970BC4195351E CRC64;		

[illegible]

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Qy 176 LQCVLTVNGANVHARACGRFQKQGCCTCYFGEPLPLSLAACKQMDVSYLLENPHOP 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177 LQCVLTVNGANVHARACGRFQKQGCCTCYFGEPLPLSLAACKQMDVSYLLENPHOP 236
Qy 236 ASLQATDSQNGTVLHALVMSIDNSAENIALVTSMTDGLQAGARLCPVVOLEDIRNLQDL 295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 ASLEATDGLGTVLHALVMSIDNSAENIALVTSMTDGLQAGARLCPVVOLEDIRNLQDL 296
Qy 296 TPLKLAKEGKIEIFRHLQREFSG-LSHLRKTETMCYGPVRSVLYDLASVDSCEENSV 354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 297 TPLKLAKEGKIEIFRHLQREFSGVQPLSRKFTETMCYGPVRSVLYDLASVDSCEENSV 356
Qy 355 LEITAFHCKSPRRHRMNVLEPLNKLQAKMDLIPKFFLNLCLNTIYFIFTAAVHOPT 414
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 357 LEITAFHCKSPRRHRMNVLEPLNKLQAKMDLIPKFFLNLCLNTIYFIFTAAVHOPT 416
Qy 415 LKQAPLKLKAEVGNMMLTGIIILGIGIYLVGLQVLPFMRHVFETISFDSFEITL 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 417 LDQPAIPSSKATFEGSMILLGHILLGLGITYLLQGLMYFMRRLFIWISFDSTFEITL 476
Qy 475 LFOALLTVVSOVLCPLATEWYLPPLVSAVLGWLNLTYTRGFQHTGYSVMIQKVLIRD 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 477 LQGLLVLSQVLRMRETEWLPPLVSLVGLWNLTYTRGFQHTGYSVMIQKVLIRD 536
Qy 535 LLRFLILTVLFGFAVALVLSLOEAMRPEAPTPGNATESVQPMGQDEGNGAQRGL 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 537 LLRFLILTVLFGFAVALVLSLOEAMRPEAPTPGNATESVQPMGQDEGNGAQRGL 594
Qy 595 EASLELFFETIGMGLAEOBOLHFRGMVLLLLAVLLTYLLMLTALMSEVNSVAT 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 595 DASLELFFETIGMGLAEOBOLHFRGMVLLLLAVLLTYLLMLTALMSEVNSVAT 654
Qy 655 DSWSMWLKOKAISYLEMENGWYWC-RKKORAGVMTLVGTPKSPDERMCFVEEENNAS 713
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 655 NSMSIMWLKOKAISYLEMENGWYWCRRKKHRSRLKVGTRGGTDERMCFVEEENNAS 714
Qy 714 WEQTLPTLCEDPSGAGVPTLENPVLASPPKEDDGASEENVVQOL 760
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 715 WEQTLPTLCEDPSGAGVPTLENPVLASPPKEDDGASEENVVQOL 757

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RESULT 7
035433 PRELIMINARY; PRT; 838 AA.
AC 035433;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VANILLOID RECEPTOR SUBTYPE 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96007969; PubMed=9349813;
RA Caterina M.J., Schumacher M.A., Tominaga M., Rosen T.A., Levine J.D.,
RT Julius D.;
RT "The capsaicin receptor: a heat-activated ion channel in the pain
    pathway".
RL Nature 389:816-824(1997).
DR EMBL; AF029310; AAC53398.1; -.
DR InterPro; IPR002110; -.
DR InterPro; IPR002111; -.
DR Pfam; PF00023; ank. 3.
DR PROSITE; PS50088; ANK_REPEAT. 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION. 1.
DR SMART; SM00248; ANK. 1.
SQ SEQUENCE 838 AA; 94947 MW; DAFCS08012BDF71BF CRC64;

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Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;
Qy 18 GOEDSEADRGKLDPSGSLPPMESQFOGEDRRKFAPOIRVN---LNYRKGTC----- 65
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 51 GKQSEAS-----PLDCPYEEGLASCPILIVSSVLTIGRGDDPASYRPSQ 99
Qy 66 ----ASQDPNRFDRDLFNVAVSRCVPEDLAGPEYLSKTSKYLTDSYTGSGTGKTCM 121
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 100 DVSAGKRPRLYDRRSIFDVAQSNCOELSLPFLQRSKKRLDSEFKDPETGKTCM 159
Qy 122 KAVILNKGVAACLPILQIDRDSGNPQPLVNAQCTDDYVGHSHALAIKRSLOQCKL 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 KAMLLHNGQDITALLLDVAKTKDSLQOFVNASYTSYVGGYALHAIERRNNTVTL 219
Qy 182 LVENGANVHARACGRFQKQGCCTCYFGEPLPLSLAACKQMDVSYLLENPHOPASLOA 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 220 LVENGADVQAANAGFFKKTGRGPFYFGEPLPLSLAACKTNOLATYKFLQMSQPADISA 279
Qy 241 TDSQGNTVLHALVMSIDNSAENIALVTSMTDGLQAGARLCPVVOLEDIRNLQDLTPLK 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 280 RDSVGNFVLAHLEVAADVTNTEKVTSMYNEILLGAKLHPTLKEITRKRKGLPLAL 339
Qy 301 AAKBKIEIFRHLQREFSG-LSHLRKTETMCYGPVRSVLYDLASVDSCEENSVLEI 358
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 340 AASSGKIGVLAITLQREHEPCCRHLRKTETMAVGPVHSSLYDSCIDTEKNSLVEI 399
Qy 359 AF-HCKSPRRHRMNVLEPLNKLQAKMDLIPK-FPLNFCNLTYMFIPTAAVHOPTLK 416
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 400 AYSSEPTNRRDMLVEPLNKLQAKMDLIPKRIYFNFVYCLMIFITAAVYRVP-- 457
Qy 417 KQAPD-HLKAEGVGNMMLTGIIILGIGIYLVGLQVLPFMRHVFETISFDSFEITL 474
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 458 -EGLPYKIKMTVGVGFYFVTEGELISVSGGVYFFFGIYFLQRRSLKSLFVDSYEITL 516
Qy 475 LFOALLTVVSOVLCPLATEWYLPPLVSAVLGWLNLTYTRGFQHTGYSVMIQKVLIRD 534
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 517 FVQSEMLVSVVLYFSQREYVAVSVFSLAGWNLMLTYTRGFQHTGYSVMIQKVLIRD 576
Qy 535 LLRFLILTVLFGFAVALVLSLOEAMRPEAPTPGNATESVQPMGQDEGNGA----- 588
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 577 LCREFEVLVLFQGSTAVVTLIED-----GN---NSLPMSTPHKRGSKACRGN 625
Qy 589 QYRGILEASLELFFETIGMGLAEOBOLHFRGMVLLLLAVLLTYLLMLTALMSET 648
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 626 SYNLSYSTCLELFTTIGMGLAEOBOLHFRGMVLLLLAVLLTYLLMLTALMSET 685
Qy 649 VNSVATDSMSIMWLKOKAISYLEMENGWYWC-RKKORAGVMTLVGTPKSPDERMCFVE 707
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 686 VNKIAQESKNIMLQORAITITLDTKSFLLCKMKKAFRSKLLQVGTTPGKDDYRMCFRVD 745
Qy 708 EVNNAWMEQTLPTLCEDPSGA-GVPTLENPVLASPPKEDDGASEENVVQOLQ 762
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 746 EVNNTWTMTNNGIINEDPGNCEGVRTLSFLRS-----RVSGRWKMKFALVPLLR 797

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RESULT 8
09JMS7 PRELIMINARY; PRT; 838 AA.
ID 09JMS7;
AC 09JMS7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VANILLOID RECEPTOR TYPE 1 LIKE PROTEIN 1.
GN VRIL1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsutsumi S., Nakamura A., Kohama K.;
RT "Vanilloid receptor type 1 like protein 1.";
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AB040873; BAA94307.1; -
 DR InterPro: IPR002110; -
 DR InterPro: IPR002111; -
 DR Pfam: PF00023; ank; 3.
 DR PROSITE: PS50088; ANK_REPEAT; 1.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR SMART: SM00248; ANK; 1.
 DR Receptor.
 SQ SEQUENCE 838 AA; 94964 MW; EE33CEAA606C3404 CRC64;

Query Match 41.3%; Score 1652; DB 11; Length 838;
 Best Local Similarity 46.3%; Pred. No. 8e-122;
 Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;

QY 18 GQDSEADGKIDFGSGLPMSQFQGEGRKAPQIRVN---LNRKKG- 65
 DB 51 GKGDSEAS-----PLDCPYEEGLASCPITVSVLTQRPDGPASVRSQ 99
 QY 66 ---ASQDPNRPDRDLFNAVSRGVPEDLAGPEYLSKTSKYLTDESEYEGSGKTCIM 121
 DB 100 DVSAGEKPPRLYDKRSIFPAVANSQCELESILPLQSRKRLTDSFQDPETGKTCL 159
 QY 122 KAVLNKDGYNACITPLLDIDRSGNPQPLVNAQCTDDYRGHSALHAIERKSLOCVKL 181
 DB 160 KAMLNJHNGQNTITALLDVARKDSLKFVNASVYDSYKGGTALHAIERNMTLVTL 219
 QY 182 LVNGANVHARAGRGFFQGG--TCFYFGLPLSLACTQMDVSYLLENPHQPSLOA 240
 DB 220 LVNGADVQAAANGDFPKKRGPFEGELPLSLAQTQALIVFELQNSQPADISA 279
 QY 241 TDSQGTVLHALVMIIDNSAENIALVTSWYDGLQAGARLCPTVOLEDIRNLDLPPLK 300
 DB 280 RDSVGTVLHALVEADVNDTNRKFTSMKNELLIGAKHPLKLEITNRKGLPPLAL 339
 QY 301 AAKEGIEIFRHLQREF--SGLSHSRKFTWCYGRVSLYDLASVDSCEENSVLEIT 358
 DB 340 AASSGKIGVLAAYLQREIHEPECRHLRSRKFTENAYGVPVSHSLYDSCIDCEKNSVLEVI 399
 QY 359 AF-HCKSPHRRVLEPLNKLQAKMDLLIPK-FELNFCNLIMYFIETAVAYHOPTLK 416
 DB 400 AVSSSTPNRHDMLVEPLRLQDKMDRFVKRIFFNFVYCYLMIFFMAAYRPV-- 457
 QY 417 KQAP--HLKAENGSMILGHTLILGLIYLVQGLWYFRRHVFIMISFIDSEFELL 474
 DB 458 -EGLPPYKLTNTGDFYRFTGELISVSGVYFPFGIQYLRPRLSKSLFVDSYSLIF 516
 QY 475 LFOALLTVVSQVLCFLAIEYLFPLVLSALVGLNLITRGTHGITSVMIOXYLRD 534
 DB 517 EVQSLFMVSVVLYFQSRKEYVASWFSIAMGWTNMLYTRGFOMGIVAMTEKMLRD 576
 QY 535 LRFELIYVLELFGFVALVLSQSEAMRPEAPTPGNATESVOPMEQDEGNGA----- 588
 DB 577 LCFMRYVYLFVLFGEFTAVVTLIED-----GKN---NSLPMESTPHKCRSACKPGN 625
 QY 589 QYRGILEASLELKFPTIGMGLAFQOLHFRGNVLLLLAVLYLTILLNMLIALMSET 648
 DB 626 SYNSLSTGCELEKFTIGMDLEFENYDKKAVFIILLAVLYLTILLNMLIALMGER 685
 QY 649 VNSVAIDNSIMKLOKALISVLEMGYWMW-RRKQRAQVMLVTGRPDGSPDERKCFRVE 707
 DB 686 VNKIADESKRMVLOKALITLDEKSFLLCMKRAFRSGKLQVFPDGDVDMWCFRVD 745
 QY 708 EVWMASMEQTLPTLCEDPSGA-GVPRTLNPVLSAPKDEDEGASEENVYVOLLO 762
 DB 746 EVWMTWNTWNTVGINEDPGNCEGVKRTLSFLRSG---RVSGRMKNKFAVPLLR 797

RESULT 9
 ID 09H304 PRELIMINARY: PRT: 839 AA.
 AC 09H304;
 DT 01-MAR-2001 (TREMBLrel, 16, Created)

DT 01-MAR-2001 (TREMBLrel, 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel, 16, Last annotation update)
 DE CAPSACIN RECEPTOR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cortright D.N., Peck A., Zou T.;
 RT "Cloning and characterization of the human capsacin receptor, VR1.";
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF196175; AAG43466.1; -
 DR Receptor.
 SQ SEQUENCE 839 AA; 94968 MW; EA9BF7D6023EPF4 CRC64;

Query Match 41.2%; Score 1651.5; DB 4; Length 839;
 Best Local Similarity 48.5%; Pred. No. 8e-122;
 Matches 344; Conservative 122; Mismatches 199; Indels 45; Gaps 11;

QY 74 FDDRLFNARVSRGVPEDLAGPEYLSKTSKYLTDESEYEGSGKTCIMKAVMLKPGVNA 133
 DB 113 YDRSIFEAVAQNNCODLESILLFLQSKKHLTDNEFKDEPKETKTLKAMLMHDGQNT 172
 QY 134 CILPLQIDRDSGNPQPLVNAQCTDDYRGHSALHAIERKSLOCVKLVENGANVHARA 193
 DB 173 TIFLELARQDTSLKELVNASTDSYIKQTRALHAIERNALYTLLENKADYQAAA 232
 QY 194 CGRFQFGOG-TCFYFGLPLSLACTQMDVSYLLENPHQPSLOANDSGNTVLHML 252
 DB 223 HGDFKTKRGPFYFGEGLPLSLAQTQALIVFELQNSQPADISARDSVPTVLHAL 292
 QY 253 VMISDMSAENIALVTSWYDGLQAGARLCPTVOLEDIRNLDLPPLKAKBKEIEFPH 312
 DB 293 VEADVNTAOTKFTVSMYELMLGAKLHPTLKLELTNNKGMTPLALAGTGKIVLAV 352
 QY 313 ILQREFS--GLSHSRKFTWCYGRVSLYDLASVDSCEENSVLELIAF-HCKSPHRR 369
 DB 353 ILQRELOEPCRLSLSKFTFEMAAGPVHSSLYDSCIDCEKNSVLEVIASSETPTNRHD 412
 QY 370 MVVLEPLNKLQAKMDLLIPK-FELNFCNLIMYFIETAVAYHOPTLKQAPDHLKAE-V 427
 DB 413 MLVEPLNRLQDKMDRFVKRIFFNFVYCYLMIFFMAAYRPV---DGLPPFMEXI 469
 QY 428 GNSMLTGHLLILGLIYLVQGLWYFRRHVFIMISFIDSEFELLFQALLTVVSQV 487
 DB 470 GDFRYVTGELISVSGVYFPFGIQYLRPRLSKSLFVDSYSLIFLQSLFMLATVYL 529
 QY 488 CFLAIEMYPLVLSALVGLNLITRGTHGITSVMIOXYLRDLRFLIYLVPLF 547
 DB 530 YFHLKEVYASWFSIALGWTNMLYTRGFOGIGIYAVMEKMLLDLCRFMYIYVPLF 589
 QY 548 GFAVALVLSQEA-----WRPAPTPGNATESVOPMEQDEGNGAORYGLI 594
 DB 590 GFSTAVVTLIEDKNDLSESTSHRWGPACRPDSS-----YNSYV 632
 QY 595 EASLELKFPTIGMGLAFQOLHFRGNVLLLLAVLYLTILLNMLIALMSETVSVAF 654
 DB 633 STCELEKFTIGMDLEFENYDKKAVFIILLAVLYLTILLNMLIALMGETVAKIA 692
 QY 655 DWSIMKLOKALISVLEMGYWMW-RRKQRAQVMLVTGRPDGSPDERKCFRVEENMAS 713
 DB 693 ESKNIMKLOKALITLDEKSFLLCMKRAFRSGKLQVYTPDGKXDYRMCFRDEVNMT 752
 QY 714 WEOGTLPCLCEDPSGA-GVPRTLNPVLSAPKDEDEGASEENVYVOLLO 762
 DB 753 WNTWGIINEDPGNCEGVKRTLSFLRSG---RVSGRMKNKFAVPLLR 798

RESULT 10
 ID 09H09 PRELIMINARY: PRT: 839 AA.
 AC 09H09;
 DT 01-MAR-2001 (TREMBLrel, 16, Created)

AC Q9H0G9; 2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
 DE HYDROTHERMAL 94.9 KDA PROTEIN.
 GN DKE2P434K0220.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Otenwaelder B., Obermaler B., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 KW EMBL: AL16801; CAB66735.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 839 AA; 94950 MW; EA9BF7D603AE4760 CRC64;

Query Match	41.2%;	Score 1648.5;	DB 4;	Length 839;
Best Local Similarity	48.5%;	Pred. No. 1.5e-121;		
Matches 344;	Conservative 122;	Mismatches 199;	Indels 45;	Gaps 11;

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OY 74 FDRDLFLNANSGVGEDLAGLEPYLSKTSKYLTDEEYSGTGKICMLKAVNLKDGVA 133
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 YDRSRIFEFVANNONQODLESILLFLQKSKKHLITDNEFDPEIGKICLKLAMLNHDGQAT 172
OY 134 CILPLLOIDRODSGNPOPLVNAOCTDDYTRGSHALHAIERKSLOCYKLLVENGANYHARA 193
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 TIFLLELTAIRQDSLKEIYLVANASYTSYGGQATLHAIERRMALVLTLLVENGADVOQANA 232
OY 194 GCRFFOKGOG--CFEFGELPLSLACFQOMDVSVLLENPHQPASLOATDSGNTVHAL 252
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 223 HODFFKTKRGREGFELPLSLACTNOLGYIKVELLONSWOTADISARDSGNTVHAL 292
OY 253 VMSIDNSAENIALVTSMTDGLLOAGARCLPTVOLEDIRNLODLPKLAAEKGIETFRH 312
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 293 VEVAANTADNMTKFVTSMTNEIILILAKLHPRLTKEELTKKGMTPLALAAIGKIGVLAY 352
OY 313 ILOREFS--GLSHSRKTEMCYGVVRVSLYDLASVDSEENSYLEITAF--HCKSPHRIR 369
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 353 ILQREIOEPCRHLSRKTEEMAYGVHSSLDSDICDEKSVLEVLAVSSSETPNRND 412
OY 370 MVLVEPLRLKLOAKMDLLIPK--FPLNFCLNIYMEIFTAVAAYHOEPLTKOAPNHLKAE--V 427
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 413 MLVLEPLRLKLOAKMDRKYRKIFRYFNELPYLCIMIIITMAAYRYR--DGLPRKMEKI 469
OY 428 GNSMLLTGHLILLCGITYLLVGOLYFEMRHVFIWISFDYSFEILLFQALLTVVSOVL 487
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 470 GDYFVTEIILSVLGGVYFFERGIQYFLQRRPSMTLLFEDYSSEMLFLOSILFMATVVL 529
OY 488 CFLALEWLPPLVLSALVIGMLNLKYTTGFOHTGYSVWIOKVIIRDLIRPLILVPLF 547
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 530 YFSHLKEYVASVFSALGWTMLYTRGFOQMGITAYVMIEMILRLDCREFPVITVPLF 589
OY 548 GFAVALVLSLOEA-----WRDEAPGTGNATESVOPMEGODEGNGAORYGITL 594
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 590 GFSTAVVTLIEDGKNDLSPESETSHRMGAPACRPDSS-----YNSLY 632
OY 595 EASLELFEFTIGMGLAQEOELHFRGMVLLILLAVALITYLLMLTALMSEYVNSVAT 654
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 633 STCLLEFETFTIGMGLEETENDEFAVPLITILLAVILITYLLMLTALMSEYVNTKLAQ 692
OY 655 DWSMILLOKALISVLEMENGYWMC--RKQORAGVMITVGKPKDGSFDERWCFEVEENMNAS 713
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 693 ESKNIMKLORAITLIDTEKSFCLKARAPRSCKLLOVGYTPDGKXDYHRCFVDEVNMTT 752
OY 714 WEQTLPTLCEDPSGA--GYPRITLENVLA SPRREDEGASSENYVYQLO 762
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 753 WNTNGIITENGDNGCEGVKRTLSFSLRSS---RVSGRMKKMFAVLVPLRL 798

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RESULT	11		
Q9NQ74			
ID	Q9NQ74	PRELIMINARY;	PRF: 839 AA.
AC	Q9NQ74;		
DT	01-OCT-2000 (TrEMBLrel, 15, Created)		
DT	01-OCT-2000 (TrEMBLrel, 15, Last sequence update)		
DT	01-MAR-2001 (TrEMBLrel, 16, Last annotation update)		
DE	VANILLOID RECEPTOR 1.		
GN	vr1.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kelsell R.E.;		
RU	Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.		

Submitted (APR-2000) to the EMBL/GenBank/DBJ databases

RT "Cloning and functional expression of a human orthologue of rat
RT vanilloid receptor-1."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277028; CAB95729.1; -.
DR InterPro; IPR002110; -.
DR InterPro; IPR002111; -.
DR Pfam; PF000023; ank; 3.
DR PROSITE; PSS0088; ANK_REPEAT; 1.
DR PROSITE; PSS0297; ANK_REP_REGION; 1.
DR SMART; SM00248; ANK; 1.
KW Receptor.
SQ SEQUENCE 839 AA; 94923 MW; 7142FFAE43189ECC CRC64;

Query Match	41.1%	Score 1644.5	DB 4	Length 839
Best Local Similarity	48.5%	Pred. No. 3,1e-121		
Matches 344	Conservative 121	Mismatches 200	Indels 45	Gaps 11
QY	74	FDRLFLNVAASRGVPEDLAFLPEYLKTSKYVLTDSYETGSGTKCLAKAVNLKGVNA	133	
Db	113	YDRRSIFEAFAVQNNQDLESLLFLFQKSKHLDNEFDPEQKCTLLKAMLNDHGNT	172	
QY	134	CILPLLOIDROSGNQPLVYNAQCTDDYRGHSALHAIATEKRSIQCVKLIVENGAVHARA	193	
Db	173	TIPLLLELTARODSIKELVYNAASYDSYKGGQALHAIATERKMAVTLTLVYENGAVQANA	232	
QY	194	CGRFQKQGG--TCEYFEGELPLSLACTQOMDVYVSLLENPHQPSAQATDSOGNTVHAL	252	
Db	233	HGDFEKKTKRGRRGFYEGELPLSLACTNQGLIVKFLQNSMQTADISARDSVGNVTVHAL	292	
QY	253	VMSINSAMENALVYMSWDGLLOAGARCLPTVQLEDINLODTPLTKLAAGKGLIEIRRH	312	
Db	293	VEVANATADNKRFEVYMSNEILLIGAKHLPTLKLEELTNKGMPTLALAAAGTGKGVLAY	352	
QY	313	ILQREFS--GLSHLSRKTYEMCGYGVRAVSLYDLAASVDCSEMSVLEIIAF--HCKSPHRRH	369	
Db	353	ILQREIQPECRHLSRKTYEMAGVPHVSSLYDLSCIDPCKEKSYLEVIAYSSSETPNRHD	412	
QY	370	MVYLEPLKLKLLQAKDILLPK--FELNFCNLTYMIFPAVAYHOPTLKKQAAPHKAE--V	427	
Db	413	MLLVEPLRLRLQDKMDRCKRVKRIFFENFLVYLCYLMIFPMAAYRVV---DGLPPKMKYT	469	
QY	428	GNSMLTLGHILILGGATILVGOALYEMRRHVFIIWISFISYFELLFQOALLTVVVSOL	487	
Db	470	GDFYRVGEILLVYLGGVYFFFRGIOYFLQRRPSMKTLFVDSSEMLFLQSLFMATAVVL	529	
QY	488	CFLALEMYLPLVLSALVYGLMNLTYTTFGFOHTGYSVMIQKIVLRDLRLFLIYVLEF	547	
Db	530	YFSHKEVVAASVMSLAGTMMYLTITGTFQOMGIYAVIAEMKLIRDLCKRMFEVYVLEF	589	

QY	548	GRAVALVLSISQEA-----WREAPATGPATSTSVQPMEEQEDEGNAQVRGLL	594
DB	590	GFSTVAVVLLIEGKDNDLSESTSHRMKGPACRPDS-----YNSLY	632
QY	595	EASLELFEKTIQMGELAFQEOHLFRQAVLLLLAVVLLTYTLLNMLIALMSETVNSVAT	654
DB	633	STCLELFEKTIQMGDELFENTYDFKAVFTILLIAYVLLTYTLLNMLIALMGVTKIAQ	692
QY	655	DSWSTWKLQKALSVLEMENGYMMC-RKKRQAGVMLTVGTRKPDGSPDERKCFRVEEYNNAS	713
DB	693	ESKNWTKLQALATVLLIDTEKSFILCMKAPRSKLLQVGTGPKGKDYRMCFRFDEVNMTT	752
QY	714	WEOTPLTECDPSGA-GVPRTELENPLVAPSPKEDEGASEEYVVPOLLO	762
DB	753	WNTNNGIINEDPGNCEGVKRTLSFSLRS-----RVSGRMKKFPALVPLLR	798
RESULT	12		
Q9NY22	09NY22	PRELIMINARY;	PRT; 839 AA.
AC	09NY22:		
DT	01-OCT-2000	(TREMBlrel. 15, Created)	
DT	01-OCT-2000	(TREMBlrel. 15, Last sequence update)	
DT	01-MAR-2001	(TREMBlrel. 16, Last annotation update)	
DE	VANILLOID RECEPTOR 1.		
GN	VRL.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=DORSAL ROOT GANGLION;		
RA	McIntyre P., Winter J., Phillips E., Webb M., Chambers A.,		
RA	Weerasekera N., Kang H., Savidge J., Clarke M., James I., Bevan S.,		
RA	McLachlan L.,		
RT	"Pharmacological comparison of human and rat VRL expressed in CHO		
RT	cells."		
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.		
RL	EMBL: AJ272063; CAB89866.1; -.		
DR	InterPro: IPR002110; -.		
DR	InterPro: IPR002111; -.		
DR	Pfam: PF00023; ank; 3.		
DR	PROSITE: PS50088; ANK_REPEAT; 1.		
DR	PROSITE: PS50297; ANK_REPEAT_REGION; 1.		
DR	SMART: SM00248; ANK; 1.		
KW	SEQUENCE.		
SO	839 AA; 94939 MW; CC0D93A3AAD725F8 CRC64;		
Query Match	40.9%; Score 1636.5; DB 4; Length 839;		
Best Local Similarity	48.2%; Pred. No. 1,3e-120;		
Matches 342; Conservative 122; Mismatches 201; Indels 45; Gaps 11.			
QY	74	FDRDLFNVAVSHGVEDLAGLPEYLSKTSKYLLTDSSETGSTGCTCLMKAVLNLDKGVNA	133
DB	113	YDRSRISFEAVANNQCNODESLFLFLQKSKHLLTDFNEFKDPETIGKTCLLAKMLNLDGGNT	172
QY	134	CLLPLLQIDRDSGNGQPLVNAOCTDDYIRGHSAHLHAIKRSIQCKLLVENGANYHARA	193
DB	173	TLPILLELAIARQDSLEKELVNASYDSYKQGTALHAIERRMVALVTLLVENGADVQANA	232
QY	194	CGRFQKOGG--TCFPEFGLPLSLACTKQMDVVSYLENPHQPASLQATDSOGNPLVHAL	252
DB	233	HGDFKRTKRGRCGYFGELPLSLACTNOLGIVKFLQSMQWOTADISARDSVGNVTLHAL	292
QY	253	WISDNSAENIALVTSMTDGLQAGARLCPTVQLEDIRNLQDLPKLKAAGKGIETIFRH	312
DB	293	VEVADNTADNFTKFTVSMYEIILIGAKLHPLTLKLELTNNKKGMPLALAAAGTGIGVLAY	352
QY	313	ILQRFPS--GLSHLSRKFTKCYGKVRVSLYDLASVDSCEENSYLETIAF-HKSPHRHR	369

QY	DB	Query Match	Best Local Similarity	36.6%, Score 1467, DB 13, Length 852, Matches 338; Conservative 121; Mismatches 245; Indels 106; Gaps 14;
QY	370	MYVLEPLNKLLDAKDDLLIPK-FELNELCNLIYMFIFFAVATHOPLKQAAPHLKAE-V	41.7%; Pred. No. 3.3e-107;	
DB	413	MLLVEPLNKLQDKMDRFVKRIEYFNFLVYCLMTIFMAAAYRPV--DGLPPKMEKT		
QY	428	GNSMLTGHILLILGCIYLVGLQWYFMRBRHFIWISFIDSEYFELLFEOALLTVASQVL		
DB	470	GDYFNVTGILLISLVGGVYFFRRGRIQYFLQKRSMKTLFSEMLFLOSLPMLATVLF		
QY	488	CFLAIEWLPLLVGLVGLWMLNLIYYTGFOHTGIYSWATOKVILLRDLRFLLIYLVLF		
DB	530	YFSHKEVYASVAFSLAIGWTMLTYTRGFOGMGYAVAMEIKMILLRDLRFMYIVYLF		
QY	548	GPAVALVLSQDA-----WREAPDTGNATSVQPMGEODEGAGQYRGTL		
DB	590	GFSTAVVILLIEGRKNDLSLPSESTSHRWKGPACRPDDSS-----YNSLY		
QY	595	EASLELEFFETTGMEIAFOEQLHFRGMVLLLLAVVLLTYILLNMLIALMSETVNSVAT		
DB	633	STCLLEFFETTGMEIAFOEQLHFRGMVLLLLAVVLLTYILLNMLIALMSETVNSVAT		
QY	655	DSMSIWKLOKATSVLEMENGYMMC-RKKORAGVMLTVGKPGSDERKCFVEEYVNNAS		
DB	693	ESKNWKLOKATSVLEMENGYMMC-RKKORAGVMLTVGKPGSDERKCFVEEYVNNAS		
QY	714	WEOTLPTECDPSGA-GVPTRELENVLAAPPEDDEGASEEYVPEVOLLO		
DB	753	WMTNVGIINDEPGNCEGVKRTLSFLRSR---RVSGRWKMKFALVPLLR		
RESULT 13				
Q9DFS3		PRELIMINARY; PRT; 852 AA.		
AC	09DFS3			
DT	01-MAR-2001	(TREMblrel. 16, Created)		
DT	01-MAR-2001	(TREMblrel. 16, last sequence update)		
DT	01-MAR-2001	(TREMblrel. 16, last annotation update)		
DE		VANILLOID RECEPTOR-RELATED OSMOTICALLY ACTIVATED CHANNEL PROTEIN.		
GN		VR-OAC.		
OS		Gallus gallus (Chicken).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC		Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC		Gallus.		
OX		NCBI_TaxID=9031;		
RN		[1]		
RP		SEQUENCE FROM N.A.		
RC		TISSUE=COCHLEA;		
RX		PubMed=11081638;		
RA		Liedtke W., Choe Y., Marti-Renom M.A., Bell A.M., Dents C.S., Sali A.,		
RA		Hudspeth A.J., Friedman J.M., Heller S.,		
RT		"Vanilloid Receptor-Related Osmotically Activated Channel (VR-OAC), a		
RT		Candidate Vertebrate Osmoreceptor.";		
RL		Cell 103:525-535(2000).		
EMBL		AF261883; AAG28026.1; -		
DR		Receptor.		
KN		SEQUENCE 852 AA; 96197 MW; E85365D3FAD08C1 CRC64;		
SO				

Db 157 SFLTHKRLDDEERESTGKTCIPKALLNLSSAGRNTIPILDIAEKTGMREFINSP 216
Qy 156 CTDYRGHSALHIAIERKSLQCVKLLVNGANGANHARACGRFFO-KGOGTCFFEGELPLS 214
Db 217 FRDYVYRGOTAHIAIERCKHYVELLVEKGDADVAQAARGFOROKDGGYVFEGLPLS 276
Qy 215 LAACRKQMDVSYLLENHOPASLOATDSOGNTVHALVMSIDNASENIALVTSMDGL 274
Db 277 LAACNPHIHYLLENHOKADLRDORSRGNTVHALVALADNNTRENTKFTKMYDILL 336
Qy 275 OAGARLCCTVOEDIRNLODLPKLAKEGKIEFRRHILDRFS--GLSHLSRKFTEMC 332
Db 337 IKCAKLPFDNLNEALLNDGSLPLMAAKTGKIGTFDHIIRRELDDEDEVRHLRSFKDMA 396
Qy 333 YGPAVNSLYDLASVDSO--EENSVELEIIAFHCKSPHRHBMVLEPLKLLOAKWDL-IPK 390
Db 397 YGPVYSSLYDLSLDTCGEVSVLEIIVYNSKIEHRHMLAVEP INELLROKMRFGAVS 456
Qy 391 FFLNPLCLNLIYFTTAVAYHOPPLKQAAPHLKAEGNSMLTGHILLLGGIYLLVGQ 450
Db 457 FYISVSVYLCAMIIPTLLAYYRP--MEGPPPYPTTYTIDYLRALAGEIITLLTGILFFESN 514
Qy 451 LM-YFMRHVFIMISFIDSYFELLFPQALLTVYSQVLCFLAIEYRLLVLSALVGLN 509
Db 515 IKDLPMKCPGVNSFFIDGSLFOLLFYISVLYTAGLVGVEAYLAVMFAVALLGMMN 574
Qy 510 LLYYRGHTGIYSVMIOKYLRLDRLFLIYVLFGLFAVALVSL-----SQE 559
Db 575 ALYFRGKLKLTGYSIMOKILFKDLFRLLVYLFLMIGVSALVSLNPPCSSSCSD 634
Qy 560 AMRPAAPPGPNATESVOPMEGOEDGNGAOYRGILASLELFFKTIGMELAFOROLHR 619
Db 635 HSNCTLPYPCSDS-----QTFSTFLDLFKLTIGMDLEMLESAXP 678
Qy 630 GMVILLIAYVLYTILLNMLIAMSETVNSVATDSIMKLOAIVLEMEY--WMC 678
Db 679 GVFIILLIYIIFVLLNMLIAMGETVGVSKSHIMKLOATVILLIDERSFPL 738
Qy 679 RKKORAGVMLTVGTGPDSPDERMCFRVEEVWMAAMEOTLPTLCDDPSGAG----- 729
Db 739 RRAFSGEMVYVKGCTDTPDRMCFRVDYVMSHMNONGIISDPKSDIYYQYGFSH 798
Qy 730 -----VPTLENPVLAAPKED 746
Db 799 TVGRLRDRMSTVVRVVE--LNKSCPTED 826
RESULT 14
Q9HBCO PRELIMINARY; PRT; 871 AA.
AC Q9HBCO;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE OTRPCA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RENAL CORTEX;
RX PubMed=11025659;
RA Strothmann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.;
"OTRPC4, a nonselective cation channel that confers sensitivity to
RT extracellular osmolarity".
RL Nat. Cell Biol. 2:695-702(2000).
DR EMBL; AF258465; AAG16127.1;
SQ SEQUENCE 871 AA; 98294 MM; C62056B86DEA6FB6 CRC64;

Query Match 36.6%; Score 1467; DB 4; Length 871;
Best Local Similarity 43.1%; Pred. No. 3.4e-107;

Matches 339; Conservative 114; Mismatches 246; Indels 88; Gaps 16;
Qy 8 PVFRLETLDDGOEDS-----SEADRCK-LDFSGSLPMESEOFGEEDRKPAF----- 52
Db 32 PLSSLANLFEQ-EDGSLSPRADASRPAGPGDGRNLMMKRGAGRKVPIDLESTL 90
Qy 53 -----QIRVNLNRYK-----GTASQDPP--NRPD 75
Db 91 YESSVVPKPAKMDSLPDYGYTRHSSDNKWRKIIIEKOPQSPKAPAPPPILLKVFN 150
Qy 76 RDRLFNAVSRGPEDLAPLEPLSTKSYLTDSEXTGCTGKMLKVVNLKQDVNCCI 135
Db 151 RPILEFDIVSRGSTADLDGLPPLTHKRLDDEERESTGKTCIPKALLNLSSAGRNTI 210
Qy 136 LPLQIDDDSGNPPPLVNAOCTDYRGHSALHIAIERKSLQCVKLLVNGANGANHARACG 195
Db 211 PYLLDIAERTGMREFINSPFRDIYRGOTAHIAIERCKHYVELLVAQGDADVAQAARG 270
Qy 196 RFPQ-KGOGTCFFEGELPLSLAECTQMDVVSYLENPHOPASLOATDSOGNTVHALVM 254
Db 271 RFPQKDEGGEYFEGELPLSLAECTQPHIIVYLTENPHKADMRDORSRGNTVHALVA 330
Qy 255 ISDNASENIALVTSMDGLDQAGARLCPTVOEDIRNLODLPKLAKEGKIEFRRIL 314
Db 331 IADNTRNTKFTVTKYDILLKCARLPDPSNLEAVLNNDGSLPLMAAKTGKIGTFDHI 390
Qy 315 QREFS--GLSHLSRKFTEMCYGPVNSLYDLASVDSO--EENSVELEIIAFHCKSPHRHBMV 371
Db 391 RREVDEOTRHLRSRKFMAVGPVSSLYDLSLDTCGEASVLEIIVYNSKIEHRHML 450
Qy 372 VLEPINKLLLOAKWDL-IPKFFLNPLCLNLIYFTTAVAYHOPPLKQAAPHLKAEGNS 430
Db 451 AVEPINELLROKMRFGAVSEYINVSYLCAVITFLAYYQPL--EGTPPYPTTYDY 508
Qy 431 MLTGHILLLIGIYLLVGLM-YFMRHVFIMISFIDSYFELLFPQALLTVYSQVLCF 489
Db 509 LRLAGEVITLFGVLEFFNTIKDLFMKCPGVNSLFDIGSFOLLFYISVLYSALVYL 568
Qy 490 LAIEYRLLPLVASALVGLMNLTYRGFOHGIYSVMIOKYLRLDRLFLIYVLFGLF 549
Db 569 AGIEYLVAVMFAVALLGMMNLITFRGLKLTGYSIMOKILFKDLFRLLVYLFLMIGY 628
Qy 550 AVALVSL-----SQEAMRPAAPPGPNATESVOPMEGOEDGNGAOYRGILASLE 599
Db 629 ASALVSLNPPCANMKVCNEDQNTCTVPTVPCSDS-----EFSTFL---LD 672
Qy 600 LFKPTIGMELAFOROLFRGVNLLLLAYVLYTILLNMLIAMSETVNSVATDSMSI 659
Db 673 LFKLTIGMDLEMSSTRYPVVFILLIYIIFVLLNMLIAMGETVGVSKSHI 732
Qy 660 WKLOKAISVLEMEY--WMCRRKORAGVMLTVGTGPDSPDERMCFRVEEVWMAAMEOTL 718
Db 733 WKLOMATIILLIDERSFVFLKRAFSGEMVYVKGSSDTPDRMCFRVDYVMSHMNONGI 792
Qy 719 PTLCEDP 725
Db 793 GIINEDP 799
RESULT 15
Q9ER28 PRELIMINARY; PRT; 871 AA.
AC Q9ER28;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE VANILLOID RECEPTOR-RELATED OSMOTICALLY ACTIVATED CHANNEL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX PubMed-11081638;
 RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
 RT Sall A., Hudspeth A.J., Friedman J.M., Heiler S.;
 "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
 candidate vertebrate osmoreceptor.";
 RL Cell 103:525-535(2000).
 DR EMBL: AF263521; AAG28027.1; -
 KW Receptor.
 SQ SEQUENCE 871 AA; 98009 MW; 5D50684DA08C34B CRC64;

Query Match 36.6%; Score 1465.5; DB 11; Length 871;
 Best Local Similarity 40.4%; Pred. No. 4.5e-107;
 Matches 341; Conservative 128; Mismatches 257; Indels 119; Gaps 16;

OY 8 PVRRLETLGGGEGDS-----EADRGKLDGSGLPMEGSGFQGEDRKRFAP-----52
 DB 32 PLSLANTFEGEGSSSLSPVDASR--PAGPGDRPMLRMKFGGAFRKGVPNPIDLESTL 90
 OY 53 -----QIRVNLNRYRKGTSASQDPDPR-----FD 75
 DB 91 YESSVYPGKKKAPMDSLFDYGTIRHHPSDKKRRKRYVEKQPOSPPKAPAPQPPPIIKVFN 150
 OY 76 RDRLEFNAVSGVPEDLAEPYLKSTSKYLTDSEYEGSTGKTCLMKAVLNKQGVNACI 135
 DB 151 RPIILFDIVSRGSTADLDGLSTYLLTHKKRLTDEPREPSTGTCLPKALLNLSGRNDTI 210
 OY 136 LPLLQIDRDSGNQPLVNAOCTDYYRGSHALIAIEKRSLOCYKLLVENGANVHARAG 195
 DB 211 PYLLDIAERTGNRKEINSFRIYRGOTALHAIERCKHYVELLIVAGADVHAQARG 270
 OY 196 RFQO-KGQGTCEYFGEPLSLACTKQMDVSYLLENPNOPASLOATDSOGNTVLHALV 254
 DB 271 RFQOPDEGTYFEGELPLSLACTNQHPIVNTLENPHKKADMRDSDSGNTVLHALVA 330
 OY 255 ISDNSAENIALVTSMDGLLQAGARLCPVYLEDIRNLQDLPELKLAEKGIETFRHIL 314
 DB 331 IADNTRENTKEVTKMYDLKLLKCSRLFPDSNLETVLINDGLSPLMAAKTGKIGVFQHI 390
 OY 315 QRFES--GLSHLSKRTFEMCYGPRVSLYDLASVDSG--EENSYLETIAFRCKSPHRRMV 371
 DB 391 RREVTDEDTRHLSRKPKDMAYGVSLSLDTGCEVSVLETLVYNSKIENHEML 450
 OY 372 VLEPLKLKLOAKWDL-IPKFFLNFCLNIYMFIFTAFAVYHOPTLKKQAPHLKAEVNS 430
 DB 451 AVPEINELLRDKRRKRGANSFYINVSYLCAMYIFTLAYQPL--EGTPPIYRTTVDY 508
 OY 431 MLTGHILLLGGIYLLVGLW-YFWRRHVFYIWSFIDSYFEILLFLOALLTVVSOVLCE 489
 DB 509 LRLAGEVITLLTGVLFFETSIKDLFMKKCPGVNSLFVDSFQLLYFYISLVVVSALYL 568
 OY 490 LAIEWLPLVLSALVGLMLLYTRGFQHTGIYSVMIOKVIILRLRLILYLVLEGF 549
 DB 569 AGIEAVLAVVFLVIGMNNALYFTRGKLKTGYTSIMQIKLEKDLFRFLVYLLFMIGY 628
 OY 550 AVALVSL-----SOEAWRPEAPGTGNATESYQPMEGDEGNGAQYRGILFASLE 599
 DB 629 ASALVTLLNPCRMMKVCNEDQSNCTVPSYPACDS-----ETFSAFI--LD 672
 OY 600 LKFTTIGMGLAFQEOJHFRGVLILLAYVLLTYILLNMLTALMSETVNSVATDSWSI 659
 DB 673 LFLTLTGMGLDEMLSSAKYPVYFILLVYIILTFVLLNMLALMGFTYGVQSKESKHI 732
 OY 660 WKLOKAIISVLEMENGY-AMCRKKQKQAGVMLJVGFKPDGSPDERKCFRVEEVNASKWEQTL 718
 DB 733 WKLOMATTTILDIERSPVFLRKAFRSGEMTYGKSSDGTDPDRRMCFRVEDVNNSHNOML 792
 OY 719 PTLCEPDS-----GAGVPRTELENPVILASPKDEDEGASEENVY 756
 DB 793 GIINEDPGKSEIYQYGFSHTMGLRLDRRMSVPRVVE-----LNKNGTDEVVV 843

OY 757 PVQLL 761
 DB 844 PLDNL 848

Search completed: July 18, 2001, 16:00:08
 Job time: 136 sec

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